SEQUENCE LISTING

<110> AKIRA MATSUMOTO

<120> Human Brain Carboxypeptidase B

<130> MAT-101PCT

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<150> JP 1999-125169

<151> 1999-04-30

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 1573

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (18)..(1097)

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att gtt ctc ttc tgt gag cag cat gtc ttc gcg ttc cag agt ggc caa    98
Ile Val Leu Phe Cys Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln
             15                  20                  25

gtt cta gct gct ctt cct aga acc tct agg caa gtt caa gtt cta cag   146
Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln
         30                  35                  40

aat ctt act aca aca tat gag att gtt ctc tgg cag ccg gta aca gct   194
Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala
     45                  50                  55

gac ctt att gtg aag aaa aaa caa gtc cat ttt ttt gta aat gca tct   242
Asp Leu Ile Val Lys Lys Lys Gln Val His Phe Phe Val Asn Ala Ser
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gat gtc gac aat gtg aaa gcc cat tta aat gtg agc gga att cca tgc   290
Asp Val Asp Asn Val Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys
                 80                  85                  90
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agt gtc ttg ctg gca gac gtg gaa gat ctt att caa cag cag att tcc 338
Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser
95 100 105

aac gac aca gtc agc ccc cga gcc tcc gca tcg tac tat gaa cag tat 386
Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr
110 115 120

cac tca cta aat gaa atc tat tct tgg ata gaa ttt ata act gag agg 434
His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg
125 130 135

cat cct gat atg ctt aca aaa atc cac att gga tcc tca ttt gag aag 482
His Pro Asp Met Leu Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys
140 145 150 155

tac cca ctc tat gtt tta aag gtt tct gga aaa gaa caa aca gcc aaa 530
Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys
160 165 170

aat gcc ata tgg att gac tgt gga atc cat gcc aga gaa tgg atc tct 578
Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser
175 180 185

cct gct ttc tgc ttg tgg ttc ata ggc cat aat cga atg tgg aga aag 626
Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys

190 195 200

aac cgt tct ttc tat gcg aac aat cat tgc atc gga aca gac ctg aat 674
Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn
205 210 215

agc aac ttt gtc tcc aaa cac tgg tgt gag gaa ggt gca tcc agt tcc 722
Ser Asn Phe Val Ser Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser
220 225 230 235

tca tgc tcg gaa acc tac tgt gga ctt tat cct gag tca gaa cca gaa 770
Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu
240 245 250

gtg aag gca gtg gct agt ttc ttg aga aga aat atc aac cag att aaa 818
Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys
255 260 265

gca tac atc agc atg cat tca tac tcc cag cat ata gtg ttt cca tat 866
Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr
270 275 280

tcc tat aca cga agt aaa agc aaa gac cat gag gaa ctg tct cta gta 914
Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val
285 290 295

gcc agt gaa gca gtt cgt gct att gac aaa act agt aaa aat acc agg 962
Ala Ser Glu Ala Val Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg
300 305 310 315

tat aca cat ggc cat ggc tca gaa acc tta tac cta gct cct gga ggt 1010
Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly
320 325 330

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Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser
335 340 345

aac cca cct gta gag aag ctt ttg ccg ctg tct cta aaa tagcttggca 1107
Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser Leu Lys
350 355 360

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<212> PRT

<213> Homo sapiens

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Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln Asn Leu Thr Thr Thr
35 40 45

Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala Asp Leu Ile Val Lys
50 55 60

Lys Lys Gln Val His Phe Phe Val Asn Ala Ser Asp Val Asp Asn Val

65 70 75 80

Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys Ser Val Leu Leu Ala

85 90 95

Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser Asn Asp Thr Val Ser

100 105 110

Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu

115 120 125

Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu

130 135 140

Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val

145 150 155 160

Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile

165 170 175

Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu

180 185 190

Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr

195 200 205

Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn Ser Asn Phe Val Ser

210 215 220

Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr

225 230 235 240

Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala

245 250 255

Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met

260 265 270

His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser

275 280 285

Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val

290 295 300

Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His

305 310 315 320

Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile

325 330 335

Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu

340 345 350

Lys Leu Leu Pro Leu Ser Leu Lys
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<210> 3

<211> 338

<212> PRT

<213> Homo sapiens

<400> 3

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Val Gln Val Leu Gln Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp
20 25 30

Gln Pro Val Thr Ala Asp Leu Ile Val Lys Lys Lys Gln Val His Phe
35 40 45

Phe Val Asn Ala Ser Asp Val Asp Asn Val Lys Ala His Leu Asn Val
50 55 60

Ser Gly Ile Pro Cys Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile
65 70 75 80

Gln Gln Gln Ile Ser Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser

85 90 95

Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu

100 105 110

Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys Ile His Ile Gly

115 120 125

Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys

130 135 140

Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala

145 150 155 160

Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn

165 170 175

Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile

180 185 190

Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His Trp Cys Glu Glu

195 200 205

Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro

210 215 220

Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn

225 230 235 240

Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His

245 250 255

Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu

260 265 270

Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala Ile Glu Lys Thr

275 280 285

Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr

290 295 300

Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys

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Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser

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Leu Lys

<210> 4

<211> 246

<212> PRT

<213> Homo sapiens

<400> 4

Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr
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Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys
20 25 30

Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys
35 40 45

Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys
50 55 60

Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe
65 70 75 80

Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn
85 90 95

Asn His Cys Ile Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His
100 105 110

Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys

115 120 125

Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe

130 135 140

Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser

145 150 155 160

Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser

165 170 175

Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala

180 185 190

Ile Glu Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser

195 200 205

Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp

210 215 220

Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu

225 230 235 240

Leu Pro Leu Ser Leu Lys

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized oligopeptide sequence

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Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu
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Asn Pro Thr Tyr Lys Phe Phe Glu
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<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

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gcctccgcat cgtactatga acagtatcac 30

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 7

ggttcatagg ccataatcga atgt 24

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially

synthesized primer sequence

<400> 8

tcaggggcat taaacattcc taat 24

<210> 9

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized oligopeptide sequence

<400> 9

Ser Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser Leu Lys

1 5 10